

Amendment to the Claims:

Please amend the claims as follows.

Please cancel claims 24 to 39, 42 to 66 and 86 to 92, without prejudice.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): An isolated or recombinant nucleic acid comprising a sequence ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and variants thereof~~ having at least about 50% sequence identity to SEQ ID NO:21, and complementary sequences thereof, SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and encoding a polypeptide having a phosphatase activity.

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Claim 2 (currently amended): The isolated or recombinant nucleic acid of claim 1, comprising a sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, sequences substantially identical thereto, and sequences complementary thereto.~~

Claim 3 (currently amended): An isolated or recombinant nucleic acid at least 20 residues in length that hybridizes to a nucleic acid of claim 1 under conditions of high stringency that include a wash under conditions including 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C, wherein hybridization is carried out at a temperature of between about 15°C to 25°C below the T<sub>m</sub>.

Claim 4 (currently amended): An isolated or recombinant nucleic acid at least 20 residues in length that hybridizes to a nucleic acid of claim 1 under conditions of moderate stringency that include a wash under conditions including 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour.

Claim 5 (currently amended): An isolated or recombinant nucleic acid at least 20 residues in length that hybridizes to a nucleic acid of claim 1 under conditions of low stringency

that include a wash under conditions including 2X SSC, 0.1% SDS at room temperature for 15 minutes.

Claim 6 (currently amended): An isolated or recombinant nucleic acid having at least about 55% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 7 (currently amended): An isolated or recombinant nucleic acid having at least about 60% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 8 (currently amended): An isolated or recombinant nucleic acid having at least about 65% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 9 (currently amended): An isolated or recombinant nucleic acid having at least 70% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 10 (currently amended): An isolated or recombinant nucleic acid having at least about 75% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 11 (currently amended): An isolated or recombinant nucleic acid having at least 80% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 12 (currently amended): An isolated or recombinant nucleic acid having at least about 85% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 13 (currently amended): An isolated or recombinant nucleic acid having at least 90% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 14 (currently amended): An isolated or recombinant nucleic acid having at least about 95% sequence identity ~~homology~~ to a [[the]] nucleic acid [[of]] as set forth in claim 1 as determined by analysis with a sequence comparison algorithm.

Claim 15 (currently amended): The isolated or recombinant nucleic acid of claim 1, ~~2, 6, 7, 8, 9, 10, 11, or 12~~, wherein the sequence identity is determined by analysis with ~~comparison algorithm~~ is FASTA version 3.0t78 with the default parameters.

Claim 16 (currently amended): An isolated or recombinant nucleic acid comprising at least [[10]] 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, sequences substantially identical thereto, and sequences~~ complementary thereto.

Claim 17 (currently amended): An isolated or recombinant nucleic acid having at least about 50% sequence identity ~~homology~~ to at least 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~the nucleic acid of claim 10~~ as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

Claim 18 (currently amended): An isolated or recombinant nucleic acid having at least about 55% sequence identity ~~homology~~ to at least 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~the nucleic acid of claim 10~~ as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

Claim 19 (currently amended): An isolated or recombinant nucleic acid having at least about 60% sequence identity ~~homology~~ to at least 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~the nucleic acid of claim 10~~ as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

Claim 20 (currently amended): An isolated or recombinant nucleic acid having at least about 65% sequence identity homology to at least 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~the nucleic acid of claim 10~~ as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

Claim 21 (currently amended): An isolated or recombinant nucleic acid having at least 70% sequence identity homology to at least 20 consecutive bases of a sequence as set forth in SEQ ID NO:21 ~~the nucleic acid of claim 10~~ as determined by analysis with a sequence comparison algorithm or FASTA version 3.0t78 with the default parameters.

Claim 22 (currently amended): An isolated or recombinant nucleic acid encoding a polypeptide having a sequence as set forth in SEQ ID NO:30 ~~selected from the group consisting of SEQ ID NOS: 28, 29, 30, 31, 32, 33, 34, 35, 36, 42, 43, 44, 46, 47, 48, 50, 52, 54, and sequences substantially identical thereto.~~

Claim 23 (currently amended): An isolated or recombinant nucleic acid encoding a polypeptide comprising at least ~~[[10]]~~ 20 consecutive amino acids of a polypeptide having a sequence as set forth in SEQ ID NO:30 ~~selected from the group consisting of SEQ ID NOS: 28, 29, 30, 31, 32, 33, 34, 35, 36, 42, 43, 44, 46, 47, 48, 50, 52, 54, and sequences substantially identical thereto.~~

Claims 24 to 39 (canceled)

Claim 40 (currently amended): A method of producing a polypeptide having a sequence as set forth in SEQ ID NO:30, or a sequence encoded by a nucleic acid as set forth in claim 1, selected from the group consisting of SEQ ID NOS: 28, 29, 30, 31, 32, 33, 34, 35, 36, 42, 43, 44, 46, 47, 48, 50, 52, 54, and sequences substantially identical thereto comprising introducing ~~[[a]]~~ the nucleic acid ~~encoding the polypeptide~~ into a host cell under conditions that allow expression of the polypeptide ~~and recovering the polypeptide.~~

Claim 41 (currently amended): A method of producing a polypeptide comprising at least 10 amino acids of a sequence as set forth in SEQ ID NO:30, or a sequence encoded by a

nucleic acid as set forth in claim 1, selected from the group consisting of SEQ ID NOS: 28, 29, 30, 31, 32, 33, 34, 35, 36, 42, 43, 44, 46, 47, 48, 50, 52, 54, and sequences substantially identical thereto comprising introducing [[a]] the nucleic acid encoding the polypeptide, operably linked to a promoter, into a host cell under conditions that allow expression of the polypeptide and recovering the polypeptide.

Claims 42 to 66 (canceled)

Claim 67 (currently amended): A nucleic acid probe comprising an oligonucleotide from about 10 to 50 nucleotides in length and having an area of at least 10 contiguous nucleotides that [[is]] has at least 50% sequence identity complementary to a nucleic acid target region [[of the]] comprising a nucleic acid sequence as set forth in SEQ ID NO:21, or its complementary sequence, selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

Claim 68 (currently amended): The probe of claim 67, wherein the oligonucleotide comprises a [[is]] DNA or an RNA.

Claim 69 (currently amended): The probe of claim 67, which [[is]] has at least 55% sequence identity complementary to the nucleic acid target region.

Claim 70 (currently amended): The probe of claim 67, which [[is]] has at least 60% sequence identity complementary to the nucleic acid target region.

Claim 71 (currently amended): The probe of claim 67, which [[is]] has at least 65% sequence identity complementary to the nucleic acid target region.

Claim 72 (currently amended): The probe of claim 67, which [[is]] has at least 70% sequence identity complementary to the nucleic acid target region.

Claim 73 (currently amended): The probe of claim 67, which ~~[[is]]~~ has at least 75% sequence identity ~~complementary~~ to the nucleic acid target region.

Claim 74 (currently amended): The probe of claim 67, wherein the oligonucleotide comprises a sequence which is 80% sequence identity ~~complementary~~ to the nucleic acid target region.

Claim 75 (currently amended): The probe of claim 67, which ~~[[is]]~~ has at least 85% sequence identity ~~complementary~~ to the nucleic acid target region.

Claim 76 (currently amended): The probe of claim 67, wherein the oligonucleotide comprises a sequence which ~~[[is]]~~ having at least 90% sequence identity ~~complementary~~ to the nucleic acid target region.

Claim 77 (currently amended): The probe of claim 67, which ~~[[is]]~~ has at least 95% sequence identity ~~complementary~~ to the nucleic acid target region.

Claim 78 (original): The probe of claim 67, which is fully complementary to the nucleic acid target region.

Claim 79 (currently amended): The probe of claim 67, wherein the oligonucleotide is 15-50 bases in length.

Claim 80 (currently amended): The probe of claim 67, wherein the probe further comprises a detectable isotopic label.

Claim 81 (currently amended): The probe of claim 67, wherein the probe further comprises a detectable non-isotopic label selected from the group consisting of a fluorescent molecule, a chemiluminescent molecule, an enzyme, a cofactor, an enzyme substrate, and a hapten.

Claim 82 (currently amended): A nucleic acid probe comprising an oligonucleotide from about 15 to 50 nucleotides in length and having an area of at least about 20

[[15]] contiguous nucleotides that is at least 90% complementary to a nucleic acid target region of the nucleic acid sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and~~ which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

Claim 83 (currently amended): A nucleic acid probe comprising an oligonucleotide from about 15 to 50 nucleotides in length and having an area of at least about 20 [[15]] contiguous nucleotides that is at least 95% complementary to a nucleic acid target region of the nucleic acid sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and~~ which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

Claim 84 (currently amended): A nucleic acid probe comprising an oligonucleotide from about 15 to 50 nucleotides in length and having an area of at least about 20 [[15]] contiguous nucleotides that is at least 97% complementary to a nucleic acid target region of the nucleic acid sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53, and~~ which hybridizes to the nucleic acid target region under moderate to highly stringent conditions to form a detectable target:probe duplex.

Claim 85 (currently amended): A nucleic acid ~~polynucleotide~~ probe for isolation or identification of phosphatase genes having a sequence which is the same as or fully complementary to a sequence as set forth in SEQ ID NO:21 ~~selected from the group consisting of SEQ ID NOS: 19, 20, 21, 22, 23, 24, 25, 26, 27, 37, 38, 39, 40, 41, 43, 45, 47, 49, 51, 53.~~

Claim 86 to 92 (canceled)

Claim 93 (new): The isolated or recombinant nucleic acid of claim 3, wherein the nucleic acid is at least 25 residues in length.

Claim 94 (new): The isolated or recombinant nucleic acid of claim 93, wherein the nucleic acid is at least 30 residues in length.

Claim 95 (new): The isolated or recombinant nucleic acid of claim 94, wherein the nucleic acid is at least 35 residues in length.

Claim 96 (new): The isolated or recombinant nucleic acid of claim 95, wherein the nucleic acid is at least 40 residues in length.

Claim 97 (new): The isolated or recombinant nucleic acid of claim 96, wherein the nucleic acid is at least 50 residues in length.

Claim 98 (new): The isolated or recombinant nucleic acid of claim 97, wherein the nucleic acid is at least 75 residues in length.

Claim 99 (new): The isolated or recombinant nucleic acid of claim 98, wherein the nucleic acid is at least 100 residues in length.

Claim 100 (new): The isolated or recombinant nucleic acid of claim 99, wherein the nucleic acid is at least 150 residues in length.

Claim 101 (new): The isolated or recombinant nucleic acid of claim 17, wherein the nucleic acid is at least 25 residues in length.

Claim 102 (new): The isolated or recombinant nucleic acid of claim 101, wherein the nucleic acid is at least 30 residues in length.

Claim 103 (new): The isolated or recombinant nucleic acid of claim 102, wherein the nucleic acid is at least 35 residues in length.

Claim 104 (new): The isolated or recombinant nucleic acid of claim 103, wherein the nucleic acid is at least 40 residues in length.



Claim 105 (new): The isolated or recombinant nucleic acid of claim 104, wherein the nucleic acid is at least 50 residues in length.

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Claim 106 (new): The isolated or recombinant nucleic acid of claim 105, wherein the nucleic acid is at least 75 residues in length.

Claim 107 (new): The isolated or recombinant nucleic acid of claim 106, wherein the nucleic acid is at least 100 residues in length.

Claim 108 (new): The isolated or recombinant nucleic acid of claim 107, wherein the nucleic acid is at least 150 residues in length.

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